

GenCore version 5.1.7
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OM protein - protein search, using SW model.

Run on: May 4, 2006, 14:33:28 ; Search time 30.061 Seconds

(without alignments)
2310.222 Million cell update/sec

Title: US-09-361-652-1

Perfect score: 4485

Sequence: 1 MLFWAAHLLSLQLVYCWA P.....NNTHFQASIQDYTRCGTT 840

Scoring table: BLOSUM62

gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgm2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/FCTUS_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	3361.5	74.9	841	2	US-09-361-652-1	Sequence 2, Appli
2	1465.6	32.5	839	2	US-09-361-652-1	Sequence 4, Appli
3	1428	31.8	843	2	US-09-361-652-1	Sequence 1, Appli
4	1425	31.8	843	2	US-09-361-652-1	Sequence 2, Appli
5	1208.5	26.9	852	2	US-09-361-652-1	Sequence 6, Appli
6	1163.5	25.9	1059	2	US-09-361-652-1	Sequence 2, Appli
7	1147	25.8	669	2	US-09-361-652-1	Sequence 7, Appli
8	1146	25.6	1078	1	US-09-361-652-1	Sequence 7, Appli
9	1146	25.6	1078	1	US-09-361-652-1	Sequence 7, Appli
10	1146	25.6	1078	1	US-09-361-652-1	Sequence 7, Appli
11	1146	25.6	1078	1	US-09-361-652-1	Sequence 7, Appli
12	1146	25.6	1078	2	US-09-353-784-7	Sequence 7, Appli
13	1146	25.6	1078	2	US-09-353-784-7	Sequence 7, Appli
14	1146	25.6	1078	2	US-09-353-784-7	Sequence 7, Appli
15	1144.5	25.5	1085	1	US-09-495-588-5	Sequence 5, Appli
16	1144.5	25.5	1085	1	US-09-495-588-5	Sequence 5, Appli
17	1144.5	25.5	1085	1	US-09-495-588-5	Sequence 5, Appli
18	1144.5	25.5	1085	1	US-09-495-588-5	Sequence 5, Appli
19	1144.5	25.5	1085	2	US-09-495-588-5	Sequence 5, Appli
20	1144.5	25.5	1085	2	US-09-495-588-5	Sequence 5, Appli
21	1144.5	25.5	1085	2	US-09-495-588-5	Sequence 5, Appli
22	1134	25.3	1088	1	US-09-484-565-5	Sequence 6, Appli
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24	1134	25.3	1088	1	US-09-484-565-5	Sequence 6, Appli
25	1134	25.3	1088	1	US-09-484-565-5	Sequence 6, Appli
26	1134	25.3	1088	2	US-09-353-784-6	Sequence 6, Appli
27	1134	25.3	1088	2	US-09-484-719B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-361-652-1

; Sequence 2, Application US/09857427A
; Patent No. 695587

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; APPLICANT: LI, XIADONG

; APPLICANT: STALEWSKI, LENA

; APPLICANT: XU, HONG

; APPLICANT: EBETERRI, FERNANDO

; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS

; FILE REFERENCE: 078003-082558

; CURRENT APPLICATION NUMBER: US/09/897,427A

; CURRENT FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 2

; LENGTH: 841

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-361-652-1

Query Match 74.9% ; Score 3361.5 ; DB 2 ; Length 841 ;
Best Local Similarity 74.1% ; Pred. No. 9.1e-311 ;
Matches 622 ; Conservative 81 ; Mismatches 136 ; Indels 1 ; Gaps 1 ;

Qy 1 MLPPWAHL-LSIQLVYCMWPSORTESSPGFSPSLHGDCLQLAGLPLHSGCLQVHRPLVT 59
Db 1 MLLCTPLRVLQLLISCCWAFACHTESSSDFTGDLAGLPLHSGCLQVHRPLVT 60

Qy 60 SCDRDPDSFGHGHYLFOAMRPTVEINNSALLNITLGCBLYDVCBSANVYATLVLIA 119
Db 61 LCDRSCSCEFHGHYLFOAMRGLGVYEEINNSTALPNTLPTQLYDVCSDSANVYATLVLIS 120

Qy 120 LQPHHIEIORDLNRHSSKRVAFGPDNTDHAFTTAALLSPFLMLVUSPASSTVLSKAR 179
Db 121 LPQHHTIELQGDLLHYSPTLVAGPDSITNTAAALLSPFLPMVISTASSTLSVLR 180

Qy 180 KFPSFLPARTVPSDRHCVYVNVQOLQSGFGWNTISLIGSYGDLQGVQALBELAIPRGICVA 239
Db 181 QYPSFLPARTVPSDRHCVYVNVQOLQSGFGWNTISLIGSYGDLQGVQALBELAIPRGICVA 240

Qy 240 FKD1YPPSARVGPDMQSMQHLLQARTTIVVPSNRHLLARVFPFNSVVLNLTKWVVAS 299
Db 241 FKD1MPSAQYGDERNQCLMRHLAQATVYVVFISROLARVFPEFVNLNLTKWVVAS 300

Qy 300 EDWATSTYTSVTGIGTQGIGTGLVAVQROVPGLEFERSVTAAPACPSWSWCST 359
Db 301 EAWALSRHITGVPGLORIGMVLGVAIQKRAVGLKAFEEAVARADKCAPRCHKGSWCSS 360

Qy	360	NOLCRECHTPTRAMPITGAPSMSAAYRTYEAVYAVAGHLHOLLCCTSECSRGPYPPWQ	419
Db	361	NOLCREQAFMAHTMPKLUKAFTSMSSAYNAYRAYAVAHGLHOLLCASGCSRGPYPPWQ	420
Qy	420	LLQQIYKVNFLHENTVAFDDNGDTLGYDIYIADWNGPWTMFTBEITGSASLSPVLDINK	479
Db	421	LBEQHAYPHLHKDTVAENDNRDPLSSNTIANDWNGPAWTFTLGSSSTWSPIQUNINE	480
Qy	480	TKIOWHGRKNNQVPVSVCITDCLAGHHRVYVGSHICFCFBCPRACTFLMSLSELHICQPCG	539
Db	481	TKIOWHGRDNDQVPKSVCSSDCLGEHQRYVTGFHICFCFBCPRACTFLMSLDTYCQPCG	540
Qy	540	TBEPWAKPESSTCPPTVPEPLAHWEPISLVLIAANTLLLUVGTAGLPWAFHFTPVRS	599
Db	541	KEEWAPESQOTCPPTVPEPLAHWEPISLVLIAANTLLLUVGTAGLPWAFHFTPVRS	600
Qy	600	GGRLLCFMLIGSLVAGSCSFYSPFGEPTPACLLRQPLSISGPAITPLSCLTIRSFLQVII	659
Db	601	GGRLLCFMLIGSLVAGSCSFYSPFGEPTPACLLRQPLSISGPAITPLSCLTIRSFLQVII	660
Qy	660	KPSTKVPFPTYRTAQNHGAGLPVYVSSSTVHLLCITWLJMMTPRPTREYQRFPHUYLEC	719
Db	661	KPSTKVPFPTYHVNQNHGAGLPVYVSSSTVHLLCITWLJMMTPRPTREYQRFPHUYLEC	720
Qy	720	TEVNSVGPTLAFTHNILLISITPVSYLGKPLPEVNEAKCVCFTPSILLNPFVSWIAFPFTA	779
Db	721	TEVNSVGPTLAFLYGLSISAPACSYLGKPLPEVNEAKCVCFTPSILLNPFVSWIAFPFTA	780
Qy	780	SIYQGSYSLPVAVNVLAGLTLSCGFGGGYFLPKCYVILCPELNNNTBHQAISQDYTRRCGT	839
Db	781	SIYQGSYSLPVAVNVLAGLTLSCGFGGGYFLPKCYVILCPELNNNTBHQAISQDYTRRCGS	840
Qy	840	T 840	
Db	841	T 841	
RESULT 2			
US-09-897-427A-4			
; Sequence 4, Application US/09897427A			
; Patent No. 6955887			
; GENERAL INFORMATION:			
; APPLICANT: ADLER, JON ELLIOT			
; APPLICANT: LI, XIAODONG			
; APPLICANT: STAZAWSKI, LENA			
; APPLICANT: XU, HONG			
; APPLICANT: EBIEVERRI, FERNANDO			
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS			
; FILE REFERENCE: 078603-0282558			
; CURRENT APPLICATION NUMBER: US/09/897,427A			
; CURRENT FILING DATE: 2001-07-03			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 4			
; LENGTH: 839			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; US-09-897-427A-4			
Query Match Score 32.5%; Length 839;			
Best Local Similarity 39.7%; Pred. No. 2.8e-129;			
Matches 327; Conservative 123; Mismatches 344; Indels 29; Gaps 12			
31 FSLPGDFLJAGLFLSHGDCQVRAHPL - VTSQDRDPSFNGHGYHFLQAMRFTVVEIINNS 88			
27 FVPGDYLGLGLFSLHANMKGIYHNFQVPMC - REYEVYKIGNMQAMFPAVEINND 85			
89 SALLPNTITGYELVYDVCSESANYVATLRLAQLGPHIEQDLRNHSKVKYAFIGPDNT 148			
86 SSUPLGVLLGVEITDVCY1SNNVQPVLYFLAH - DMNLPQDSDYNSXSYVAVIGPDNT 144			
149 DHAVTAALLGPFMLPVTEASVSVLSACKRPPSPARTVSDRHYEVNQLLSQFGWV 208			

RESULT 3
US-09-361-631-1
; Sequence 1, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; FILE REFERENCE: 0230/B-08720US
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino

Db	145	ESWNTVANPLSLFLPQITYSAISPELRDKVRFPLLRTPSADHVEAMYVQLMHFRWN	204
Qy	209	WISLJGSGTSDYQGQVQALEBLAYERGICVAFKDVTVF-----SARVGDRMPSQSMQHL	262
Db	205	WIVLVSSDTYGRDNGQLGERVARDICIAFQETLPTLQPNQNTSEERQLVTIVDKL	264
Qy	263	AQARTTVVVFPSNRHLARVEFRSVLANTTGKVVWASEDVAISTVITTSVTSQGIGTRVLG	322
Db	265	QOSTARVVVVFSPDITLYHFFNEVRLQNFQGAVWASESAIDPVHLNLTELGHJFLFG	324
Qy	323	VAVQQRVQVGLKEFPESTYRVAAPSACPEGSWSKSTNQLCRECHTFTRAMPTLGAFSM	382
Db	325	ITIQSPVPIQFSETREWGQAGPPPLSRTSOSYTC-NQECDNCNLNATLSFNTLRLSGE	382
Qy	383	SAAYVRYRAYAYAHLGHOLLGCTSEICISRGPVYWPQLLQOIQYKWNFLHENTVAFDNG	442
Db	383	RVYVSVYSSAVAYAHLHSLGDSLSTCTKRVVYWPQLEEBIWKONTLHQIFFDPQG	442
Qy	443	DTLGYYDIAWDNGPEWPFITIGSASLSPVHLDI-NKTKLQWKGKRNQVQVPSVCTDCL	501
Db	443	DVALHLETYQWQWDRSQNQPQSV-ASYYPLQRQKRNQD1SMWHTYNTNTMMSMSKRCQ	500
Qy	502	AGHRRVVVQVSHRHCCPBCVPEBAGTFLNMSE-LHICOPCGTEBWAPEKESTTCPPRTVBLA	560
Db	501	SGQKKKPVGHVCCFECIDCLPGTFLNHTDEBQACPNNEWSQSETSCKRQLVYFLE	560
Qy	561	WHB--PISLYLIAA---NTLILLLVGTAGLFAWHFHTPVYRSAGRLCPFLMGSLSVAG	614
Db	561	WHEAPTIAVALLAAGFLSTLALIV-----IFWRFHQTPVYRSAGPMPCLMLTLLVVA	614
Qy	615	SCSFYSPFGEPTVPCPLLQPLFSGRAIFSLCJTSFOLVYIIPKFSTKVTFYRTWQ	674
Db	615	YMWVYVYVGPBKVSCLCQALPPLCFTICISCIAVRSAGPMSRPRAYSTWVR	674
Qy	675	NHGAGALFVVSSTVHLICLUTWLWVWTPR-TREYORPHVILECTEVNSVGPLLAFTH	733
Db	675	YQGPVSMAPITVLEMVIVVIGMLTGLSPTRTBDPKITIVSNCNPNTNSLFLNTSL	734
Qy	734	NIIIS1STEVCSYLGKELPENYNEAKCUTFSLLNPNFWSIAFFTMASIYQGSYLPAYVNL	793
Db	735	DLLASVVGFSFATMKGKELPNTYNEAKPITLMSMTPFPTSSVSLCTFMAYSGLVLTIVDLL	794
Qy	794	AGLTTSGLSGFSGYFPPKPKCYVILCRLPBNNTFHFOISIQLDTRR	836
Db	795	VTMVLLAISLGYPBKPKCYMFLFVYERPNTPAYFNSNQIGTMR	837

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OM protein - protein search, using SW model

Run on: May 4, 2006, 14:52:34 ; Search time 100.773 Seconds
(without alignments)

3482.855 Million cell updates/sec

Title: US-09-361-652-1

Perfect score: 4485

Sequence: 1 MLFWAHLILSLLQLVYCWAP.....NNTEHFQASIQDVTYRRCGTT 840

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6_ptoada/1/pubbaa/US08_PUBCOMB.pep.*
3: /cgn2_6_ptoada/1/pubbaa/US09_PUBCOMB.pep.*
4: /cgn2_6_ptoada/1/pubbaa/US10_PUBCOMB.pep.*
5: /cgn2_6_ptoada/1/pubbaa/US10B_PUBCOMB.pep.*
6: /cgn2_6_ptoada/1/pubbaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4485	100.0	840	3 US-09-361-652-1	Sequence 1, App1
2	4485	100.0	840	3 US-09-927-315-1	Sequence 1, App1
3	4485	100.0	840	4 US-10-246-785-3	Sequence 3, App1
4	4485	100.0	840	4 US-10-190-417-1	Sequence 1, App1
5	4485	100.0	840	4 US-10-159-339-12	Sequence 12, App1
6	4485	100.0	840	4 US-10-179-373-16	Sequence 16, App1
7	4485	100.0	840	4 US-10-436-715-39	Sequence 39, App1
8	4485	100.0	840	4 US-10-436-715-69	Sequence 69, App1
9	4485	100.0	840	4 US-10-725-103-16	Sequence 16, App1
10	4485	100.0	840	4 US-10-725-489-16	Sequence 16, App1
11	4485	100.0	840	4 US-10-725-080-16	Sequence 16, App1
12	4485	100.0	840	4 US-10-725-472A-16	Sequence 16, App1
13	4485	100.0	840	5 US-10-725-418-16	Sequence 16, App1
14	4485	100.0	840	5 US-10-679-102-1	Sequence 1, App1
15	4123	91.9	842	4 US-10-436-715-35	Sequence 35, App1
16	4123	91.9	842	4 US-10-436-715-67	Sequence 57, App1
17	4100	91.4	842	3 US-09-361-652-2	Sequence 2, App1
18	4100	91.4	842	3 US-09-927-315-2	Sequence 2, App1
19	4100	91.4	842	4 US-10-246-785-2	Sequence 2, App1
20	4100	91.4	842	4 US-10-190-417-2	Sequence 2, App1
21	4100	91.4	842	5 US-10-679-102-2	Sequence 2, App1
22	4078	90.9	842	4 US-10-436-715-68	Sequence 68, App1
23	4026.5	89.8	1138	4 US-10-261-882-4	Sequence 4, App1
24	3364	75.0	840	4 US-10-190-417-3	Sequence 3, App1
25	3364	75.0	840	5 US-10-679-102-3	Sequence 3, App1
26	3362.5	75.0	841	4 US-10-188-186-2	Sequence 2, App1
27	3361.5	74.9	841	5 US-10-885-493-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-361-652-1
; Sequence 1, Application US/09361652
; Publication No. US2003003663041
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeyer, Juergen
; APPLICANT: Ryba, Nick
; APPLICANT: Hoorn, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 023478-08610US
; CURRENT APPLICATION NUMBER: US 09/361,652
; CURRENT FILING DATE: 1999-07-27
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
US-09-361-652-1

Query Match 100.0% ; Score 4485, DB 3 ; Length 840;
Best Local Similarity 100.0% ; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPAAHLLSLLQVYCAFWPSQSCRTBSSPGFSLPGDPFLLAGFLPSLHGDCQLQVHRLPLTYS 60
Db 1 MLPAAHLLSLLQVYCAFWPSQSCRTBSSPGFSLPGDPFLLAGFLPSLHGDCQLQVHRLPLTYS 60
QY 61 CDRDPSNQHGTYHLFQAMRPTVEINNSALLPNTLGYBLDVCBSANVYATLRLVIAL 120
Db 61 CDRDPSNQHGTYHLFQAMRPTVEINNSALLPNTLGYBLDVCBSANVYATLRLVIAL 120
QY 181 FPSPLRTYPSDRICQEVYNQLOSGFWYIISLICSYGDIYQGLGVQALBEFLAVPRGICYAF 240
Db 181 FPSPLRTYPSDRICQEVYNQLOSGFWYIISLICSYGDIYQGLGVQALBEFLAVPRGICYAF 240
QY 241 KDIYPPSARVGDPDMQSMNMOHLAQARTTVVYVSNRHLARVPPSVYLANLTSKVWVASE 300
Db 241 KDIYPPSARVGDPDMQSMNMOHLAQARTTVVYVSNRHLARVPPSVYLANLTSKVWVASE 300

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OM protein - protein search, using SW model

Run on: May 4, 2006, 14:54:39 ; search time 16.0553 seconds

(without alignments)
2421.578 Million cell updates/sec

Title: US-09-361-652-1
Perfect score: 4485

Sequence: 1 MLFPAHLLSLQLVYCWAF.....NNTEHFOASIQDVTTRCGTT 840

Scoring table: BLOSUM62

Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
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2: /SIDSS5/ptodata/2/pubpa/us06_new_pub.pep.*
3: /SIDSS5/ptodata/2/pubpa/us07_new_pub.pep.*
4: /SIDSS5/ptodata/2/pubpa/us08_new_pub.pep.*
5: /SIDSS5/ptodata/2/pubpa/pct_new_pub.pep.*
6: /SIDSS5/ptodata/2/pubpa/us05_new_pub.pep.*
7: /SIDSS5/ptodata/2/pubpa/us09_new_pub.pep.*
8: /SIDSS5/ptodata/2/pubpa/us10_new_pub.pep.*
9: /SIDSS5/ptodata/2/pubpa/us10_new_pub.pep.*
10: /SIDSS5/ptodata/2/pubpa/us11_new_pub.pep.*
11: /SIDSS5/ptodata/2/pubpa/us11_new_pub.pep.*
12: /SIDSS5/ptodata/2/pubpa/us60_new_pub.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4485	100.0	840	9 US-10-645-441-1	Sequence 1, Appli
2	4485	100.0	840	9 US-10-725-475-16	Sequence 2, Appli
3	4100	91.4	842	9 US-10-645-441-2	Sequence 3, Appli
4	3361.5	74.9	841	9 US-10-725-475-5	Sequence 4, Appli
5	3361.5	74.9	841	11 US-11-050-804-2	Sequence 5, Appli
6	3154.5	70.3	777	9 US-10-645-441-3	Sequence 6, Appli
7	1456.5	32.5	839	9 US-10-725-475-6	Sequence 7, Appli
8	1456.5	32.5	839	11 US-11-050-804-4	Sequence 8, Appli
9	1445.4	32.4	838	9 US-10-645-441-9	Sequence 9, Appli
10	1428	31.8	843	9 US-10-645-441-7	Sequence 10, Appli
11	1428	31.8	843	9 US-10-725-475-17	Sequence 11, Appli
12	1425	31.8	843	9 US-10-645-441-8	Sequence 12, Appli
13	1211.5	27.0	852	9 US-10-725-475-7	Sequence 13, Appli
14	1208.5	26.9	852	9 US-10-645-441-15	Sequence 14, Appli
15	1208.5	26.9	852	11 US-11-050-804-6	Sequence 15, Appli
16	1197	26.7	858	9 US-10-645-441-25	Sequence 16, Appli
17	1197	26.7	858	9 US-10-725-475-4	Sequence 17, Appli
18	1189.5	26.5	858	9 US-10-645-441-18	Sequence 18, Appli
19	1189.5	26.4	858	9 US-10-645-441-23	Sequence 19, Appli
20	1180.5	26.3	858	9 US-10-645-441-20	Sequence 20, Appli
21	1138	25.4	867	9 US-10-725-475-19	Sequence 21, Appli

RESULT 1
US-10-645-441-1
; Sequence 1, Application US/10645441
; Publication No. US20050260599A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryb, Nicholas J. P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02-070E-120110US
; CURRENT APPLICATION NUMBER: US/10/645,441
; CURRENT FILING DATE: 2003-08-20
; PRIORITY APPLICATION NUMBER: US/09/927,315
; PRIORITY FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: US 60/302,898
; PRIORITY FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat T1R1 sweet taste receptor
US-10-645-441-1

ALIGNMENTS

22	1079	24.1	928	9 US-10-841-129-6	Sequence 4, Appli
23	1061	23.7	926	9 US-10-841-129-2	Sequence 6, Appli
24	1023	22.8	926	9 US-10-841-129-2	Sequence 2, Appli
25	731	16.3	1199	9 US-10-922-166-15	Sequence 15, Appli
26	728	16.2	845	9 US-10-922-166-15	Sequence 18, Appli
27	719	16.0	879	9 US-10-877-346-17	Sequence 17, Appli
28	714	15.9	879	9 US-10-877-346-17	Sequence 16, Appli
29	713	15.9	879	9 US-10-877-346-54	Sequence 54, Appli
30	712.5	15.9	865	11 US-11-094-519A-41	Sequence 41, Appli
31	710.5	15.8	879	9 US-10-877-346-52	Sequence 52, Appli
32	476.5	10.6	242	9 US-10-725-475-13	Sequence 13, Appli
33	447.5	10.0	497	9 US-10-918-857-8	Sequence 8, Appli
34	447.5	10.0	576	9 US-10-922-166-2	Sequence 2, Appli
35	447.5	10.0	790	9 US-10-918-857-6	Sequence 6, Appli
36	447.5	10.0	790	9 US-10-922-166-20	Sequence 20, Appli
37	388	8.7	425	9 US-10-918-857-4	Sequence 4, Appli
38	388	8.7	718	9 US-10-918-857-2	Sequence 2, Appli
39	381.5	8.5	256	9 US-10-877-346-85	Sequence 85, Appli
40	375	8.4	236	9 US-10-725-475-15	Sequence 14, Appli
41	326.5	7.3	165	9 US-10-725-475-14	Sequence 12, Appli
42	310.5	6.9	137	9 US-10-725-475-12	Sequence 81, Appli
43	284	6.3	402	9 US-10-877-346-84	Sequence 40, Appli
44	177.5	4.0	844	11 US-11-127-877-40	Sequence 2, Appli
45	165.5	3.7	885	9 US-10-912-971-2	Sequence 2, Appli

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QY	121	QGPRHIEIQKDLRHNSSKVVAFIGPDPNTDHAUTTAALIGPFLMPLYSYEASVVLSAKRK 180	
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QY	181	PPSLRITPSDRHCVENVQLLASPGFWISLIGSKDYGQLGVQALEELAVPRGCVAF 240	
QY	181	PPSLRITPSDRHCVENVQLLASPGFWISLIGSKDYGQLGVQALEELAVPRGCVAF 240	
QY	241	KD1VPSARVGDPDMQSMQHLLAQARTTVVVFNSRHLARVFRSYVLANTJGKVVVASE 300	
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QY	301	DWAIYSTYITSVTGLOGICTVLGVAVQORQVPGKLKEFEESYVRAATPSACPEGSMCSTN 360	
QY	301	DWAIYSTYITSVTGLOGICTVLGVAVQORQVPGKLKEFEESYVRAATPSACPEGSMCSTN 360	
QY	361	QLCRECHFTTRAMPGLGFSMAMARYTEAVAVANGLHQJLGSBICSRGPVYFWQL 420	
QY	361	QLCRECHFTTRAMPGLGFSMAMARYTEAVAVANGLHQJLGSBICSRGPVYFWQL 420	
QY	421	LOQIYKVNPLLHENTVAFDNGDILGYYDIADWNGPWTPEIISASLSLSPVHLDNKT 480	
QY	421	LOQIYKVNPLLHENTVAFDNGDILGYYDIADWNGPWTPEIISASLSLSPVHLDNKT 480	
QY	481	KIQPHGKQKQVQPVSVCTTDCLAGHRRVYVGSHHCFCVCPBAGTFLNMSLHLICQPCGT 540	
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QY	541	EENWPKESTTCPCPTTEFLAWHEEISLVIANTLLLLVGTAGLPAWHTTPVRSAG 600	
QY	541	EENWPKESTTCPCPTTEFLAWHEEISLVIANTLLLLVGTAGLPAWHTTPVRSAG 600	
QY	601	GRLCFLMGSVAGSCSFYSPFGEPTPACLURQPLSGLPAFLSCLTIRSFLQYTFIK 660	
QY	601	GRLCFLMGSVAGSCSFYSPFGEPTPACLURQPLSGLPAFLSCLTIRSFLQYTFIK 660	
QY	661	FSTKVPTFTRWAGHNGAGLFVTVSSTVHLICITWLYMWTPRPTREYQRPHLVILECT 720	
QY	661	FSTKVPTFTRWAGHNGAGLFVTVSSTVHLICITWLYMWTPRPTREYQRPHLVILECT 720	
QY	721	EVNSVGFLLAFTNILLSTTFCYKLGELPNYNEAKCVTPSLLANFVSHAFPTMAS 780	
QY	721	EVNSVGFLLAFTNILLSTTFCYKLGELPNYNEAKCVTPSLLANFVSHAFPTMAS 780	
QY	781	IYQQSYLPAVNTVLAGLTLSGGFEGYFLPKCFTVYLCRPELBNNTBHFOASIQDYTRRCGTT 840	
QY	781	IYQQSYLPAVNTVLAGLTLSGGFEGYFLPKCFTVYLCRPELBNNTBHFOASIQDYTRRCGTT 840	
RESULT 2 US-10-725-475-16			
; Sequence 16, Application US/10725475			
; Publication No. US20060014208A1			
; GENERAL INFORMATION:			
; APPLICANT:	ZOLLER, MARK		
; APPLICANT:	LI, XIAODONG		
; APPLICANT:	STASZEWSKI, LENA		
; APPLICANT:	O'CONNELL, SHAWN		
; APPLICANT:	ZOZULIA, SERGEY		
; APPLICANT:	ADLER, JON		
; APPLICANT:	XU, HONG		
; APPLICANT:	ECHEVERRI, FERNANDO		
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES			
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR			
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS			
; FILE REFERENCE: 078003-0391566			
; CURRENT APPLICATION NUMBER: US/10/725,475			
; CURRENT FILING DATE: 2003 12-03			
; PRIOR APPLICATION NUMBER: 60/300,444			
; PRIOR FILING DATE: 2001-07-26			
; PRIOR APPLICATION NUMBER: 60/304,749			

RESULT 2
US-09-897-427A-4
TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
FILE REFERENCE: 078003-0-082558
SEQUENCE 4, Application US/09897427A
; Patent No. 6955887
; GENERAL INFORMATION:
; APPLICANT: ADDER, JON ELLIOT
; APPLICANT: LI, XIAODONG
; APPLICANT: SPRAZENSKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: EHEVERI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
; CURRENT APPLICATION NUMBER: US/09/897,427A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-897-427A-4

Query Match 32.0%; Score 1440.5%; DB 2; Length 839;
Best Local Similarity 39.8%; Pred. No. 1.be-12%; Mismatches 341; Indels 35; Gaps 15;
Matches 329; Conservative 121; Mismatches 341; Indels 35; Gaps 15;

Qy 33 PSLPGDFDLAGLPSILADCOLVRHRPL--VTSQCDRSDFDNGCHYLQAMRPTVEEINS 90
Db 27 PVLPGDYLGGLPSILAHMKGIVHLNFQYPMC-KEYBVKTCYGNLQMAMRPAVEEIND 85

Qy 91 TALLPNITLGLEYDVCSSSISNTLYRPAQQGTGHNLQMRDLRNHSKVALIGDNT 150
Db 86 SLLIPGVNLIGYEIVDVCITSNNVQPVLLPLAHE-DNLPIQEDYSNTYSRUVVAVIGPNS 144

Qy 151 DHAUTTAALLSPPLMLPLYSYEASSVILSGRKPKPSFLRTIPSDRXYQEVIVRILQSQFW 210

RESULT 3
US-09-361-631-1
; Sequence 1, Application US/09361631
; Patent No. 6333778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindenmeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307B-08720US
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE: OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino

Db 145 ESMVTANFSLFLPLQITVSAISDELRDKYRPLRTPSADHVEAVYQMLMLHPRWN 204
Qy 211 WISLWGSYGDYQQLGVOQALEELATPRGICVAFKDQYVPL--SAQAGDPRMQRML--RL 264
Db 205 WIWLVSSDTYGRDNGQLLGVRARDDICIAFOQETLPTLQNTNQNTTSEB0RLV7TVDKL 264
Qy 265 ARARTTVVVSNSRNHLAGVPRPSVLANLTKWVAEDWATISTLTVNPQJQGIGTVLG 324
Db 265 QSTARVWVVSQDPLJLYHFTNEVRQNEFSTGAVWASEVAIDPVHLNLTEGLHGTFLG 324
Qy 325 VAIQQRQVPLKEFESYQAVMGAPRTCPGSSWCTNOLCRECHARTTWNMPLEGAFSM 384
Db 325 ITIQSVP1GFSERFEGPQA-GPPPLSRTSQSTCNCNQEDCNLNTLSPNTLRLSGE 382
Qy 385 SAAVNTYBAKTAVAVSHHQLHJGCTSETCARGPVYPMQLOQYKVNELLHCKTVAFDKG 444
Db 383 RVVSYSSAVAVAHLSLUGCDKSTCTKRVVYPMQLLBEIWKVNTFLDHOIIPDPQG 442
Db 445 DPLGYDILANDWNGPWTVEIGASLSPVHLDI-NKTKLQWGHGKONQVPUVSCTVRDCL 503
Db 443 DVALHLEIVQWDRSNSNPQSY--ASYYPQRORJNQDTSWHTYNTNTMSMCSRRCQ 500
Qy 504 EGHHLWGMGSHCCFBGMPCEAGTFLN-TSBLHTCOPCGTBEPAPGSSACPSRTVBLG 562
Db 501 SGQKKEPVGIVHCCPECIDCLPGLTFLNHTDEYECQACPNNWSYQSBTSCEFKRQVPLF 560
Qy 563 WHE--PTSLVLLAA---NTULLLJLJTAGLFAWR-LHTTPVVRAGGRGLCFLMGLSLVA 615
Db 561 WHEAPTAVALLAAGFLSTLAIWLF-----WHRFQTPIVRSAGGPMPCLMLTLLV 613
Db 616 GSCSCLYSFFGKPTVPACLLQPLPSLGRFAIPLSCLTIRSPQVLIIFKPKSTKVPFTHTWA 675
Db 614 ATMVPPVYVGPPKVSTLCRQALPFCFTICLSCVAKMASIPRAYSYWW 673
Qy 676 QNHGAGI---FVIVSSTVHLFLCULTLAMMTPRPTBEYQRPHLWILECTEVNSVGLVA 732
Db 674 RYQGPYTSMAFPTVLRMV--IVVIGMIALTGLSPTRTDPPDKITIVSCNPVNRNSLFN 731
Qy 733 FAHNLLSISPFVCSYLGKBLPENNTNEAKCVTFPSLILHFWSMIAFFTMSSIXQGSTLPAV 792
Db 732 TSLDLIISVVGPSFAMGKELPTNNEAKFTLISMPYFTTSVSLCTFMSAYSQGVLTIV 791
Qy 793 NVLAGLATLSGGFSGYFLPKCYVILCRPELANTENHQASIQDYTRR 838
Db 792 DILVTVNLALASLGFQPKCYMILYPERITPAVYNSMIGCYMR 837

Result No.	Score	Query	Match	Length	DB ID	Description
1	4504	100.0	842	3	US-09-361-652-2	Sequence 2, Appli
2	4504	100.0	842	3	US-09-927-315-2	Sequence 2, Appli
3	4504	100.0	842	4	US-10-246-785-2	Sequence 2, Appli
4	4504	100.0	842	4	US-10-190-417-2	Sequence 2, Appli
5	4504	100.0	842	5	US-10-679-102-5	Sequence 35, Appli
6	4479	99.4	842	4	US-10-436-715-35	Sequence 1, Appli
7	4455	99.4	842	4	US-10-436-715-67	Sequence 67, Appli
8	4455	98.9	842	4	US-10-436-715-68	Sequence 68, Appli
9	4100	91.0	840	3	US-09-361-652-1	Sequence 1, Appli
10	4100	91.0	840	3	US-09-927-315-1	Sequence 3, Appli
11	4100	91.0	840	4	US-10-246-785-3	Sequence 1, Appli
12	4100	91.0	840	4	US-10-190-417-1	Sequence 12, Appli
13	4100	91.0	840	4	US-10-159-339-12	Sequence 16, Appli
14	4100	91.0	840	4	US-10-179-373-16	Sequence 39, Appli
15	4100	91.0	840	4	US-10-436-715-39	Sequence 66, Appli
16	4100	91.0	840	4	US-10-436-715-69	Sequence 16, Appli
17	4100	91.0	840	4	US-10-725-103-69	Sequence 16, Appli
18	4100	91.0	840	4	US-10-725-489-16	Sequence 16, Appli
19	4100	91.0	840	4	US-10-725-080-16	Sequence 16, Appli
20	4100	91.0	840	4	US-10-725-472A-16	Sequence 16, Appli
21	4100	91.0	840	5	US-10-725-418-16	Sequence 16, Appli
22	3656.5	81.2	1138	4	US-10-679-102-1	Sequence 4, Appli
23	3448.5	74.3	841	4	US-10-726-482-4	Sequence 2, Appli
24	3449.5	74.4	841	4	US-10-188-186-2	Sequence 2, Appli
25	3448.5	74.3	841	3	US-09-819-946-2	Sequence 2, Appli
26	3448.5	74.3	841	3	US-09-897-427A-2	Sequence 2, Appli
27	3448.5	74.3	841	3	US-09-799-629-17	Sequence 17, Appli

Db 241 AFKDVVPLSAQAGDPRMMMLRLARARTTVVVFSNRLLAGYFRSFLANLTKWIA 300
 Qy 301 SEDWAISITVNVPGICIGTLYAIIQVPGUKEPEESVYQAVMGAPRTCPBEGSICG 360
 Db 301 SEDWAISITVNVPGICIGTLYAIIQVPGUKEPEESVYQAVMGAPRTCPBEGSICG 360
 Db 361 TNQLCREAHTTNNMPBAGPNSAAVNTYAVAVHGLHQLLGSGTCAKGPPW 420
 Qy 421 QLQQIYKVNFLHCKTVAFDKGDPLGTYDIIAWDNGPEWFEVIGASLSPVHLDIN 480
 Db 421 QLQQIYKVNFLHCKTVAFDKGDPLGTYDIIAWDNGPEWFEVIGASLSPVHLDIN 480
 Qy 481 KTKLQWKGKQNPVQPSVCTPDCBCHRLYMGSHCCBMPCEAGTFLNTSLHTCPC 540
 Db 481 KTKLQWKGKQNPVQPSVCTRDCLBCHRLYMGSHCCBMPCEAGTFLNTSLHTCPC 540
 Qy 541 GTEBWAEGSSACFRTVBLGWPBISLVLANTLFLLLIGTAGFPAWRLHTPVRS 600
 Db 541 GTEBWAEGSSACFRTVBLGWPBISLVLANTLFLLLIGTAGFPAWRLHTPVRS 600
 Qy 601 AGGRLCFLMGSLSVAGSCSLSYSSFGKPTVPACLLRLQPLFSLCITISFOLYI 660
 Db 601 AGGRLCFLMGSLSVAGSCSLSYSSFGKPTVPACLLRLQPLFSLCITISFOLYI 660
 Qy 661 FKESTKVPYHTWQHNGAGIPTVIVSTYHQLMAMWTRPTREYQREPHLYLE 720
 Db 661 FKESTKVPYHTWQHNGAGIPTVIVSTYHQLMAMWTRPTREYQREPHLYLE 720
 Qy 721 CTEVNSGFLVAFNILLISLISITVSCYKGELPNYEAKCTPSLLHFVSMIAFTM 780
 Db 721 CTEVNSGFLVAFNILLISLISITVSCYKGELPNYEAKCTPSLLHFVSMIAFTM 780
 Qy 781 SSIYQGSYLPVNVLAGLATLSGGFSGYLPKCYTILCRPELNTNEHQASIDYTRCG 840
 Db 781 SSIYQGSYLPVNVLAGLATLSGGFSGYLPKCYTILCRPELNTNEHQASIDYTRCG 840
 Qy 841 TT 842
 Db 841 TT 842

RESULT 2
 US-09-927-315-2
 Sequence 2, Application US/09927315
 Publication No. US20030040045A1
 GENERAL INFORMATION:
 APPLICANT: Zuker, Charles S.
 APPLICANT: Ryba, Nicholas J.P.
 APPLICANT: Nelson, Greg
 APPLICANT: Hoon, Mark A.
 APPLICANT: Chandrashekar, Jayaram
 APPLICANT: Zhang, Yifeng
 APPLICANT: The Regents of the University of California
 APPLICANT: The Government of the United States of America
 APPLICANT: As represented by the Secretary of the
 APPLICANT: Department of Health and Human Services
 TITLE OF INVENTION: Mammalian Sweet Taste Receptors
 FILE REFERENCE: 023078-120101US
 CURRENT APPLICATION NUMBER: US/09/927,315
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: US/09/927,315
 PRIOR FILING DATE: 2001-07-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 842
 TYPE: PRT
 ORGANISM: Mus musculus
 FEATURE:
 OTHER INFORMATION: mouse Tr1 sweet taste receptor

us-09-927-315-2
 Sequence 2, Application US/09927315
 Publication No. US20030040045A1
 GENERAL INFORMATION:
 APPLICANT: Zuker, Charles S.
 APPLICANT: Ryba, Nicholas J.P.
 APPLICANT: Nelson, Greg
 APPLICANT: Hoon, Mark A.
 APPLICANT: Chandrashekar, Jayaram
 APPLICANT: Zhang, Yifeng
 APPLICANT: The Regents of the University of California
 APPLICANT: The Government of the United States of America
 APPLICANT: As represented by the Secretary of the
 APPLICANT: Department of Health and Human Services
 TITLE OF INVENTION: Mammalian Sweet Taste Receptors
 FILE REFERENCE: 023078-120101US
 CURRENT APPLICATION NUMBER: US/09/927,315
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: US/09/927,315
 PRIOR FILING DATE: 2001-07-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 842
 TYPE: PRT
 ORGANISM: Mus musculus
 FEATURE:
 OTHER INFORMATION: mouse Tr1 sweet taste receptor

RESULT 3
 US-10-246-785-2
 Sequence 2, Application US/10246785
 Publication No. US20030148448A1
 GENERAL INFORMATION:
 APPLICANT: IRM, LLC
 APPLICANT: The Scripps Research Institute

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DM protein - protein search, using SW mode!

Run on: May 4, 2006, 14:54:39 ; Search time 16.0935 Seconds
(without alignments)

2421.578 Million cell updates/sec

Title: US-09-161-652-2

perfect score: 4504

Sequence: 1 MLFWAAHLLLSLQLAVAYCW.....NNTEHQAS1QDYTRRCGTT 842

Scoring table: BLOSUM62

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Seachd: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Seachd: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Qy 121 AQGQTGHLEMORDLRNHSKVVALLIGPQNTDHAVTTAALLSPFLMLPSYBASSVILSGK 180
 Db 121 AQGQTGHLEMORDLRNHSKVVALLIGPQNTDHAVTTAALLSPFLMLPSYBASSVILSGK 180
 Qy 161 RKPSFLTIPSDKQVETVIRLQSPGRWVISLVSIGDYGGLGVQALEBLATPRCIV 240
 Db 161 RKPSFLTIPSDKQVETVIRLQSPGRWVISLVSIGDYGGLGVQALEBLATPRCIV 240
 Qy 241 AFKDVVPLSAQAGDPRIMQMLRMLARATTTVVVFSSNHLAGYFRSVVLANLTGKWA 300
 Db 241 AFKDVVPLSAQAGDPRIMQMLRMLARATTTVVVFSSNHLAGYFRSVVLANLTGKWA 300
 Qy 301 SEDWAISTYTINYPGIQGIGTGTGVAIQORQVGLKBEFEETSYQAVNGCAPRTCPCEGSWCG 360
 Db 301 SEDWAISTYTINYPGIQGIGTGTGVAIQORQVGLKBEFEETSYQAVNGCAPRTCPCEGSWCG 360
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 Db 361 TNOLCRECHAFITWNMPLEGAFMSAANVYEAAYAVANGHLLQIGCTSGTCARGPPW 420
 Qy 421 QLQIQIYKVNFLIHKRTAFDDKGDPGLYDIAWDNGPENTFVGASLSPVHLDIN 480
 Db 421 QLQIQIYKVNFLIHKRTAFDDKGDPGLYDIAWDNGPENTFVGASLSPVHLDIN 480
 Qy 481 KTKIQWHKRNNOYEVSYCTRDCLEGHHRLVMGSHHCCPECMPEBAGTPLANTSBLHTCOPC 540
 Db 481 KTKIQWHKRNNOYEVSYCTRDCLEGHHRLVMGSHHCCPECMPEBAGTPLANTSBLHTCOPC 540
 Qy 541 GTEWAPESSACCSRTYFLGKHEPISVLLANTLILLIGTAGLFAMRLHTPVR 600
 Db 541 GTEWAPESSACCSRTYFLGKHEPISVLLANTLILLIGTAGLFAMRLHTPVR 600
 Qy 601 AGGRLCFLMLGSLVAGCSLVSFGKPKTPACLLRQPSLGLPAIFSLCLTRSFQVII 660
 Db 601 AGGRLCFLMLGSLVAGCSLVSFGKPKTPACLLRQPSLGLPAIFSLCLTRSFQVII 660
 Qy 661 FKFSTKVPTEYHTWAQNQAGIFIVTSSVHFLCFLTLMAMTPRPTBYQRFPHLYLB 720
 Db 661 FKFSTKVPTEYHTWAQNQAGIFIVTSSVHFLCFLTLMAMTPRPTBYQRFPHLYLB 720
 Qy 721 CTENNSGVLVAPAHNLLISITSTVCSYLGKELPENTBAKCUTFSLLHFSWIAFTM 780
 Db 721 CTENNSGVLVAPAHNLLISITSTVCSYLGKELPENTBAKCUTFSLLHFSWIAFTM 780
 Qy 781 SSIYQGSTLPDVNVLAGATLSSGFGSLPKCYVILCRLPELNTHEQASIQDYTRRCG 840
 Db 781 SSIYQGSTLPDVNVLAGATLSSGFGSLPKCYVILCRLPELNTHEQASIQDYTRRCG 840
 Qy 841 TT 842
 Db 841 TT 842

RESULT 2
 US-10-645-441-1
 Sequence 1, Application US/1065441
 Publication No. US2005026599A1
 GENERAL INFORMATION:
 APPLICANT: Zuker, Charles S.
 APPLICANT: Rypa, Nicholas J. P.
 APPLICANT: Nelson, Greg
 APPLICANT: Hoon, Mark A.
 APPLICANT: Chandrasekar, Jayaram
 APPLICANT: Zhang, Yifeng
 APPLICANT: the Regents of the University of California
 APPLICANT: The Government of the United States of America
 APPLICANT: as represented by the Secretary of the
 APPLICANT: Department of Health and Human Services
 APPLICANT: Mammalian Sweet Taste Receptors
 TITLE OF INVENTION: Mammalian Sweet Taste Receptors
 FILE REFERENCE: 023078-120110US
 CURRENT APPLICATION NUMBER: US10/645,441
 CURRENT FILING DATE: 2003-08-20

Qy 360 QIKHVKHFLIHKDTVAFNNDPDLSSSYNNTIAWDNGPKWTFVLSGSSTWSPYQVQINNETKI 419
 Db 424 QIKHVKHFLIHKDTVAFNNDPDLSSSYNNTIAWDNGPKWTFVLSGSSTWSPYQVQINNETKI 483
 Qy 420 QHIGKHNHQVKPSVCSSPCLGEHORVVTGSPFHCCFECYVCGAGTFLNKSBLYRCOPCTEE 479
 Db 484 QHIGKDNQVKPSVCSSPCLGEHORVVTGSPFHCCFECYVCGAGTFLNKSBLYRCOPCTEE 543
 Qy 480 WAEGSQCPFRTVFLALRENTSWLIAANTLILIGTAGLEAFNHLDTPVRSAGCR 539
 Db 544 WAEGSQCPFRTVFLALRENTSWLIAANTLILIGTAGLEAFNHLDTPVRSAGCR 603
 Qy 540 LCPFLMLGSLAAGGSSLYGFGBPTRPACILRQLPAQFTIFSCLTFRSFLQIITPKS 599
 Db 604 LCPFLMLGSLAAGGSSLYGFGBPTRPACILRQLPAQFTIFSCLTFRSFLQIITPKS 663
 Qy 600 TKVPTFVHAWQVNHAGLFLVMISSAAQOLLICLTMWLVTPLPAREYORPHLYMLECTET 659
 Db 664 TKVPTFVHAWQVNHAGLFLVMISSAAQOLLICLTMWLVTPLPAREYORPHLYMLECTET 723
 Qy 660 NSLGFLILFLYNGLISIISAFACSYLKGDLPEYNEAKCTPSLLENFNSWIAFPTTASVY 719
 Db 724 NSLGFLILFLYNGLISIISAFACSYLKGDLPEYNEAKCTPSLFLNFYTFWIAFPTTASVY 783
 Qy 7220 DGKYLPAAMMAGLSSSGGGYFLPLPCVILCRPDNSTEHRQASQDYTRRCGST 777
 Db 784 DGKYLPAAMMAGLSSSGGGYFLPLPCVILCRPDNSTEHRQASQDYTRRCGST 841

RESULT 2
 ; Sequence 2
 ; Sequence 1, Application US/09361631

Patent No. 6383778

GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.

; APPLICANT: Adler, Jon Elliot

; APPLICANT: Lindemer, Juergen

; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
 ; TITLE OF INVENTION: Involved in Sensory Transduction

; FILE REFERENCE: 023071B-088720US

; CURRENT APPLICATION NUMBER: US 09/361,631

; CURRENT FILING DATE: 1999-07-27

; EARLIER FILING DATE: 1998-07-28

; EARLIER APPLICATION NUMBER: US 60/095,464

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 843

; TYPE: PRT

; ORGANISM: Rattus sp.

; FEATURE:

; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino

; OTHER INFORMATION: acid sequence

; US-09-361-631-1

; PDRNSTERHQASITQDYTRR 773

; DB 823 PERNITASVFNMSIQGTMR 841

RESULT 3

US-09-897-427A-4

; Sequence 4, Application US/09897427A

; Patent No. 6955887

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; APPLICANT: LI, XIADONG

; APPLICANT: STAZEWSKI, LENA

; APPLICANT: XU, HONG

; APPLICANT: EBREVERI, FERNANDO

; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS

; FILE REFERENCE: 078003-0282558

; CURRENT APPLICATION NUMBER: US/09/897-427A

; CURRENT FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-897-427A-4

Query Match 31.1%; Score 1288; DB 2; Length 843;

Best Local Similarity 37.7%; Pred. No. 1e-120;

Matches 301; Conservative 142; Mismatches 294; Indels 62; Gaps 22;

Qy 9 GYHFOQMLGVREINNSTALLPNTIAGYOLYDVCSDSANVYATLRLVSLPGOHHTLG 68

Db 71 GYNLMQARFAVEELINNSLPLPGVLLGTYEMDVCLSNITH-----PGYFLADD 122

Qy 69 DLL-----HYSPTVLAVGPDSITRATAALLSPFLV-HISYAASETLSVKQPS 120

Db 123 DLEPLTKDYSQMPHVAVGPDSITRATAALLSPFLV-HISYAASETLSVKQPS 182

Qy 121 FLRTIPNDYQVETMVLQIQRGTTWISVGSSSDYQGLGQVALENQALVR--GICIAFK 178

Db 183 MLRTIPSPATHIEAMVQLYHQMWNWVLSDDYDRENSHLL-SQRLTKTSDCIAFQ 241

Qy 179 DIMPF--SAQV--GDERMQC--LMRHIAQAGATVYVFSSQRLARYFESVLTNLTGKV 232
 Db 242 EYLPIPESQVRSBQLDNLKURRTSARVTVPSPLSLSPPSHETVRWNNTGTV 301
 Qy 233 WYASEAWALSRHITVGYPIQIGVQIAQKRAYVGLKAPEEAAYRADKEA--PRPCHKG 291
 Db 302 WIASESWAIDPVLHNLTELRHTGTVGTVSIPGSFR--VRRDKGYPVPTNT 358
 Qy 292 SWCSNQLCREOAFWIAHTMPKLAFTS--MSS--AYNAYRAYAYAVALGHOLIGCAS 344
 Db 359 LRTTCNQDCDAC-----LNTTKSPNLLSGRVRVSYSSAYAVAHALRHLIGCNR 411
 Qy 345 BLCRSGRVYWPOLLEQIHKVHFLLKDVTAFNDNRPLOSSNLIANDWNGPKWTFVTLGS 404
 Db 412 VRCTKQKTVYWPOLLEIWHVNTFLGENRLPDDQGDMPMLLDIIQWQDLSQNPQFQIAS 471
 Qy 405 STWSPVQLNINE-TKLOWHKGKHNHOVPKSVCSSDCLEGHQRYVUTGPHCCFECVPGAGTF 463
 Db 472 -YSPTSKRLTYINNSWVYTPNNTPVSMCSKSCQPMQMKSVGLHPCCFBLDCMPGT 529
 Qy 464 LNKSLYRKQCPGCTEWAPCGSQTCPRTVFLALREHTSKW--LIAA---NTUILLL 516
 Db 530 LNRSADBFENCLSCPGSMWSYKNIDTCFQRRTPLFLEHEVPTVAVVAAALGFSTAILL 589
 Qy 517 LIGTAGLIPAWHLDTPVVRSAAGRGLCFLMGLSIAAGGSSLYGFPGFEPTRPACILRQLPAL 576
 Db 590 -----IFWHRHQTQPTVTSAGGPMCPMLVPLLAQGMPVYVGPPTVFSQCRQAFFTV 643
 Qy 577 GPTIPLSLCLTVRSFQIILIKPSTKYPTEHAWVQNHAGLFLVMISSAAQOLLICLTLWV 636
 Db 644 CPSICLCSITVRSFQIVCFVKMARRLPSSAYSFWMRTHGPTVFAPIKVALVGMMLA 703
 Qy 637 WPLLP-AREYQRPHIYMLECTETSGFLAFLYNGLSSISAFACSYLGDLPENPNEA 695
 Db 704 TTINPIGTRDPPDPNIMILSCHPNYRNLFLNTSMIDLVSQGFSFAYMGKELPNTNEA 763
 Qy 696 KCVTFSLLFNFVSWIAPPTTASVYDVKYLPKANMMAG-LSSLSGFGAGYPLBKCYTILCR 754
 Db 764 KPTLSMTPSFSSISLCTEMVSD3VLTIMDLVTVLNFLAIGL-GYFBGKCTMILFY 822
 Qy 755 PDINSTEHFQASITQDYTRR 773
 Db 823 PERNITASVFNMSIQGTMR 841

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OM protein - protein search, using SW model

Run on: May 4, 2006, 14:52:34 ; Search time 93.2147 seconds
(without alignments)
3482.855 Million cell updates/sec

Title: US-09-361-652-3
Perfect score: 4138
Sequence: 1 RSCFNEHGTHLFQAMRLGV.....NSTHFQASIQDTRRCGST 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867559 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867559

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6_ptodata/1/pubbaa/us07_pubcomb.pep:*

2: /cgn2_6_ptodata/1/pubbaa/us08_pubcomb.pep:*

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5: /cgn2_6_ptodata/1/pubbaa/us11_pubcomb.pep:*

6: /cgn2_6_ptodata/1/pubbaa/us11_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4138	100.0	777	3	US-09-361-652-3	Sequence 3, Appli
2	4138	100.0	777	3	US-09-927-315-3	Sequence 3, Appli
3	4138	100.0	840	4	US-10-190-417-3	Sequence 3, Appli
4	4138	100.0	840	5	US-10-679-102-3	Sequence 3, Appli
5	4121	99.6	777	4	US-10-225-567A-676	Sequence 67, Appli
6	4068.5	98.3	841	3	US-09-819-946-2	Sequence 2, Appli
7	4068.5	98.3	841	5	US-10-885-493-2	Sequence 2, Appli
8	4064.5	98.2	841	3	US-09-897-427A-2	Sequence 2, Appli
9	4064.5	98.2	841	3	US-09-799-629-17	Sequence 17, Appli
10	4064.5	98.2	841	4	US-10-035-045-17	Sequence 17, Appli
11	4064.5	98.2	841	4	US-10-190-417-27	Sequence 27, Appli
12	4064.5	98.2	841	4	US-10-179-373-5	Sequence 5, Appli
13	4064.5	98.2	841	4	US-10-311-196-3	Sequence 3, Appli
14	4064.5	98.2	841	4	US-10-725-081-17	Sequence 17, Appli
15	4064.5	98.2	841	4	US-10-724-223-17	Sequence 17, Appli
16	4064.5	98.2	841	4	US-10-725-103-5	Sequence 5, Appli
17	4064.5	98.2	841	4	US-10-725-489-5	Sequence 5, Appli
18	4064.5	98.2	841	4	US-10-725-080-5	Sequence 5, Appli
19	4064.5	98.2	841	4	US-10-724-222-17	Sequence 17, Appli
20	4064.5	98.2	841	4	US-10-725-472A-5	Sequence 5, Appli
21	4064.5	98.2	841	4	US-10-725-276-17	Sequence 17, Appli
22	4064.5	98.2	841	4	US-10-770-127-197	Sequence 197, Appli
23	4064.5	98.2	841	4	US-10-726-168-17	Sequence 17, Appli
24	4064.5	98.2	841	5	US-10-725-284-17	Sequence 17, Appli
25	4064.5	98.2	841	5	US-10-725-418-5	Sequence 5, Appli
26	4064.5	98.2	841	5	US-10-679-102-27	Sequence 27, Appli
27	4063.5	98.2	841	4	US-10-188-186-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-361-652-3
; Sequence 3, Application US/09161652
; Publication No. US20030036630A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon B.
; APPLICANT: Lindemeyer, Juergen
; APPLICANT: Ryba, Nick
; APPLICANT: Hoop, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307B-088610US
; CURRENT APPLICATION NUMBER: US/09/361,652
; CURRENT FILING DATE: 1999-07-27
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor B3 (GPCR-B3)
US-09-361-652-3

Query Match 100.0%; Score 4138; DB 3; Length 777;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSCFNEHGTHLFQASIQDTRRCGST 100.0%; Score 4138; DB 3; Length 777;
1 RSCFNEHGTHLFQASIQDTRRCGST 100.0%; Score 4138; DB 3; Length 777;

QY 61 QHHHLQDGLLHSSPTLAVIGPSTNRATTAAVSPPLVHISYAAASSTTLSYKQYPS 120
61 QHHHLQDGLLHSSPTLAVIGPSTNRATTAAVSPPLVHISYAAASSTTLSYKQYPS 120

QY 61 FLRTIPNDKQVETMVLQKFGMCLMRHLAQGATTVVVFSSRQLARYFESVTLNTGKWWASBWA 240
61 FLRTIPNDKQVETMVLQKFGMCLMRHLAQGATTVVVFSSRQLARYFESVTLNTGKWWASBWA 240

QY 181 MPFAQGQDGRMCLMRHLAQGATTVVVFSSRQLARYFESVTLNTGKWWASBWA 240
181 MPFAQGQDGRMCLMRHLAQGATTVVVFSSRQLARYFESVTLNTGKWWASBWA 240

QY 181 MPFAQGQDGRMCLMRHLAQGATTVVVFSSRQLARYFESVTLNTGKWWASBWA 240
181 MPFAQGQDGRMCLMRHLAQGATTVVVFSSRQLARYFESVTLNTGKWWASBWA 240

QY 241 LSRHTGVPQIQRGMVLGVAIQRAVPGIKAPEBAYARADKEAPRCPCKGSMGSNQLC 300
241 LSRHTGVPQIQRGMVLGVAIQRAVPGIKAPEBAYARADKEAPRCPCKGSMGSNQLC 300

Db 241 LSRHITGTYGIGIGMVGVAIKRRAVPGKLAPEAYARADKRAPRPPCHRGSCNSNQLC 300
 Qy 301 RECCQFMHTMPKIKAPFMSAYNAYRAYVAVAHGLQHOLGCCASELCSRGRYTPWQJLHQ 360
 Db 301 RECCQFMHTMPKIKAPFMSAYNAYRAYVAVAHGLQHOLGCCASELCSRGRYTPWQJLHQ 360
 Qy 361 IHRVHFLHDKTVAFNDRDPLSSYNTIAWDNGPKWVFTVLSSTSISPVQLNINETKIQ 420
 Db 361 IHRVHFLHDKTVAFNDRDPLSSYNTIAWDNGPKWVFTVLSSTSISPVQLNINETKIQ 420
 Qy 421 WHGRNHQVPSVCSSDCLEGHQVVTGHCFCPECGTPLANKSLYRCOPCGTBEW 480
 Db 421 WHGRNHQVPSVCSSDCLEGHQVVTGHCFCPECGTPLANKSLYRCOPCGTBEW 480
 Qy 481 APESQTCPPRTVFLALREHTSNVLLANTLILGTTAGLFLAMHLDTPVVRSAQRL 540
 Db 481 APESQTCPPRTVFLALREHTSNVLLANTLILGTTAGLFLAMHLDTPVVRSAQRL 540
 Qy 541 CPMMLGSLAAGSSLYGGFGEPRPACLRLQALPAGTTFISCLTVSPQLIIFKST 600
 Db 541 CPMMLGSLAAGSSLYGGFGEPRPACLRLQALPAGTTFISCLTVSPQLIIFKST 600
 Qy 601 KVPTFHYAVNQHAGLFWMISSAQQLICLTVLWVTPLPARYQRFPHLYMLECTEN 660
 Db 601 KVPTFHYAVNQHAGLFWMISSAQQLICLTVLWVTPLPARYQRFPHLYMLECTEN 660
 Qy 661 SLGPILAFYNGLISISAPACSYLQKDIPENTYNEAKCYTFSLIFPNFVWIAFTTASYD 720
 Db 661 SLGPILAFYNGLISISAPACSYLQKDIPENTYNEAKCYTFSLIFPNFVWIAFTTASYD 720
 Qy 721 GKLPAANMAGLSSLSGGGFLPKCIVLCPDNLSTENHQASIDYTRCGST 777
 Db 721 GKLPAANMAGLSSLSGGGFLPKCIVLCPDNLSTENHQASIDYTRCGST 777
 Db 721 GKLPAANMAGLSSLSGGGFLPKCIVLCPDNLSTENHQASIDYTRCGST 777

RESULT 2
 US-09-927-315-3
 ; Sequence 3, Application US/0927315
 ; Publication No. US20030040045A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Nelson, Greg
 ; APPLICANT: Hoon, Mark A.
 ; APPLICANT: Chandrasekhar, Jayaram
 ; APPLICANT: Zhang, Yifeng
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
 ; FILE REFERENCE: 02307B-120101US
 ; CURRENT APPLICATION NUMBER: US/09/927,315
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/302,898
 ; PRIOR FILING DATE: 2001-07-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 777
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human T1R1 sweet taste receptor
 US-09-927-315-3

Query Match 100.0%; Score 4138; DB 3; Length 777;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSCSFNEGHYLQAMRLGVBEINNSTALLPNTTGYQYDVCSDSANVYATRVLSPG 60
 Do 1 RSCSFNEGHYLQAMRLGVBEINNSTALLPNTTGYQYDVCSDSANVYATRVLSPG 60

Qy 121 FLRTIPNDKQVETMVLIIQKFGNTWISLVGSSDDYGGOLGYOALENOLVRGTCIAFPDI 180
 Db 121 FLRTIPNDKQVETMVLIIQKFGNTWISLVGSSDDYGGOLGYOALENOLVRGTCIAFPDI 180
 Qy 181 MPFSAQVCDERMOCIMRLAQAQATVUVFSSQARYFFESTVLTNTGKTYWASEWA 240
 Db 181 MPFSAQVCDERMOCIMRLAQAQATVUVFSSQARYFFESTVLTNTGKTYWASEWA 240
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 5
 ; LENGTH: 841
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-725-475-5

Qy 241 LSRHITGPGIQIGMVGVAIKRAGVGLKAPEAYRADKEAPRPHKGNCSSNQLC 300
 Db 241 LSRHITGPGIQIGMVGVAIKRAGVGLKAPEAYRADKEAPRPHKGNCSSNQLC 300

Qy 301 RECOAFMARTMPKLKAFSMSATNAYRAYAYAVHGLQOLLGCASELCSRGRYTPWOLBQ 360
 Db 301 RECOAFMARTMPKLKAFSMSATNAYRAYAYAVHGLQOLLGCASELCSRGRYTPWOLBQ 360

Qy 361 IHKVPHLHKDTYAFNDRDPLOSSNTIANDWNGPKWTFVPLGSSTSPVQLNINETKIQ 420
 Db 361 IHKVPHLHKDTYAFNDRDPLOSSNTIANDWNGPKWTFVPLGSSTSPVQLNINETKIQ 420

Qy 421 WHGKHOQPKVSSESSDCLEGHQRTVTPHCCPBCVPGAGTPLNKSELYRCOPCGTEW 480
 Db 421 WHGKHOQPKVSSESSDCLEGHQRTVTPHCCPBCVPGAGTPLNKSELYRCOPCGTEW 480

Qy 481 APEGSQTCFPTVFLAILEHTSWLVLANTLILIGTLGAFWHLDPVRSAGRL 540
 Db 481 APBSQTCFPTVFLAILEHTSWLVLANTLILIGTLGAFWHLDPVRSAGRL 540

Qy 541 CPLMLGSLAAGSSLYGFFGEPTRPACIROLFALGTTIPLSCLTVSPQLIIFPKST 600
 Db 541 CPLMLGSLAAGSSLYGFFGEPTRPACIROLFALGTTIPLSCLTVSPQLIIFPKST 600

Qy 601 KVPTFHAWQNIGAGLFTMISAAQQLICLTLVWVTPLPARYOPPHLYMLECTEN 660
 Db 601 KVPTFHAWQNIGAGLFTMISAAQQLICLTLVWVTPLPARYOPPHLYMLECTEN 660

Qy 661 SLGPFLAPLYNLISISAPACSYLGDOLPENTNEAKCVPFLSLLFNFTSWIAFTTASVYD 720
 Db 661 SLGPFLAPLYNLISISAPACSYLGDOLPENTNEAKCVPFLSLLFNFTSWIAFTTASVYD 720

Qy 721 GKYLPAANMAGLSSLSGGGFLPKCYVILCRPDNISTHENQASIDYTRCGST 777
 Db 721 GKYLPAANMAGLSSLSGGGFLPKCYVILCRPDNISTHENQASIDYTRCGST 777

Qy 721 GKYLPAANMAGLSSLSGGGFLPKCYVILCRPDNISTHENQASIDYTRCGST 777
 Db 721 GKYLPAANMAGLSSLSGGGFLPKCYVILCRPDNISTHENQASIDYTRCGST 777

Qy 420 QWHRGNEQVPKSVSSDPLEGHQRVTFGPHCCPBCVPGAGTPLNKSELYRCOPCGTE 479
 Db 484 QWHRGNDQNPQPKSVSSDPLEGHQRVTFGPHCCPBCVPGAGTPLNKSDLYRCOPCGKE 543

Qy 480 WAPEGSQTCFPTVFLAILEHTSWLVLANTLILIGTLGAFWHLDPVRSAGGR 539
 Db 544 WAPEGSQTCFPTVFLAILEHTSWLVLANTLILIGTLGAFWHLDPVRSAGGR 603

Qy 540 LCFLMLGSLAAGSSLYGFFGEPTRPACIROLFALGTTIPLSCLTVSPQLIIFPKS 599
 Db 604 LCFLMLGSLAAGSSLYGFFGEPTRPACIROLFALGTTIPLSCLTVSPQLIIFPKS 663

Qy 600 TRVPTFHAWQNIGAGLFTMISAAQQLICLTLVWVTPLPARYOPPHLYMLECTET 659
 Db 664 TRVPTFHAWQNIGAGLFTMISAAQQLICLTLVWVTPLPARYOPPHLYMLECTET 723

Qy 660 NSLGKFLAFLYNGLISISAPACSYLGDOLPENTNEAKCVPFLSLLFNFTSWIAFTTASVY 719
 Db 724 NSLGKFLAFLYNGLISISAPACSYLGDOLPENTNEAKCVPFLSLLFNFTSWIAFTTASVY 783

Qy 720 DGKYLPAANMAGLSSLSGGGFLPKCYVILCRPDNISTHENQASIDYTRCGST 777
 Db 784 DGKYLPAANMAGLSSLSGGGFLPKCYVILCRPDNISTHENQASIDYTRCGST 841

RESULT 2
 US-10-725-475-5
 ; Sequence 5, Application US/10725475
 ; Publication No. US20060014208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOLLER, MARK
 ; APPLICANT: LI, XIAODONG
 ; APPLICANT: SPASZENSKI, LENA
 ; APPLICANT: O'CONNELL, SHAWN
 ; APPLICANT: 202ULYA, SERGEY
 ; APPLICANT: ADLER, JON
 ; APPLICANT: XU, HONG
 ; APPLICANT: ECHEVERRI, FERNANDO
 ; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
 ; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
 ; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
 ; CURRENT APPLICATION NUMBER: 07/003-0291556
 ; CURRENT FILING DATE: 2003-12-03
 ; PRIOR APPLICATION NUMBER: 60/300,434
 ; PRIOR FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: 60/304,749
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: 60/310,493
 ; PRIOR APPLICATION NUMBER: 60/331,771
 ; PRIOR FILING DATE: 2001-11-21

RESULT 3
 US-11-050-804-2